OM protein - protein search, using sw model

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GenCore version 5.1.6

Run on: November 20, 2004, 16:27:40 ; Search time 94 seconds

    US-09-783-931-65

    1175.233 Million cell updates/sec

    (without alignments)

Title:
Perfect score: 1160
Sequence: 1 GFTWPGTFSLIIEALHTDSP.........CNQDLNYCTHHKPCKNGATC 192

Scoring table: BLOSUM62
    Gapop 10.0 , Gapext 0.5

Searched: 1825181 seqs, 575374646 residues

Total number of hits satisfying chosen parameters: 1825181

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
    Maximum Match 100%
    Listing first 45 summaries

Database :   Uniprot_02:*
    1: uniprot_sprot:*
    2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1160	100.0	723	1	DLl1_HUMAN	O00548 homo sapien
2	1138	98.1	728	2	Q9O656	Q9O656 gallus gall
3	1125	97.0	714	1	P97677	P97677 rattus norv
4	1122	96.7	722	1	DLl1_MOUSE	Q61483 mus musculu
5	1122	96.7	722	2	Q6PFV7	Q6pfv7 mus musculu
6	1122	96.7	722	2	AAH57400	Aah57400 mus muscu
7	1122	96.7	722	2	AAH57400	Aah57400 mus muscu
8	1122	96.7	721	2	AAZ30869	Aaz30869 mus muscu
9	1077	92.8	721	2	AAH65063	Aah65063 mus muscu
10	1074	92.6	726	2	Q91902	Q91902 xenopus lae
11	1059	91.3	717	2	Q8AW87	Q8aw87 cynops pyrr
12	1059	91.3	720	2	P87357	P87357 brachydanio
13	1054	90.9	772	2	Q8UWJ4	Q8uwj4 brachydanio
14	1054	90.9	802	2	Q6D148	Q6d148 brachydanio
15	835.5	72.0	642	2	P79941	P79941 xenopus lae
16	835.5	72.0	642	2	Q7ZXT4	Q7zxt4 xenopus lae
17	794	68.4	615	2	O57409	O57409 brachydanio
18	774.5	66.8	664	2	O57409	O57409 brachydanio
19	742.5	64.0	684	2	Q91AT6	Q91at6 brachydanio
20	709.5	61.2	685	1	DLl4_HUMAN	Q9Y219 homo sapien
21	685.5	59.1	438	2	O81497	O81497 cupiennius
22	685.5	58.7	686	1	DLl4_MOUSE	O88516 mus musculu
23	680.5	58.7	686	2	Q9J171	Q9j171 mus musculu
24	680.5	58.7	650	2	Q9DBU9	Q9dbu9 mus musculu
25	680.5	58.3	650	2	Q7QOM5	Q7qom5 anopheles g
26	676	58.3	650	2	P10041	P10041 drosophila
27	659.5	56.9	833	1	DL_DROME	P10041 drosophila
28	659.5	56.9	833	2	Q6T4M9	Q6t4m9 drosophila
29	659.5	56.9	833	2	Q6T4N0	Q6t4n0 drosophila
30	659.5	56.9	833	2	Q6T4N2	Q6t4n2 drosophila
31	659.5	56.9	833	2	Q6T4N3	Q6t4n3 drosophila
32	659.5	56.9	833	2	Q6T4N4	Q6t4n4 drosophila
33	659.5	56.9	833	2	Q6T4N6	Q6t4n6 drosophila
34	659.5	56.9	833	2	AAO25024	Aao25024 drosophil
35	659.5	56.9	833	2	AAR24453	Aar24453 drosophil
36	659.5	56.9	833	2	AAR24454	Aar24454 drosophil
37	659.5	56.9	833	2	AAR24455	Aar24455 drosophil
38	659.5	56.9	833	2	AAR24456	Aar24456 drosophil
39	659.5	56.9	833	2	AAR24457	Aar24457 drosophil
40	659.5	56.9	833	2	AAR24458	Aar24458 drosophil
41	659.5	56.9	833	2	AAR24459	Aar24459 drosophil
42	659.5	56.9	833	2	AAR24460	Aar24460 drosophil
43	659.5	56.9	833	2	AAR24461	Aar24461 drosophil
44	659.5	56.9	833	2	AAR24463	Aar24463 drosophil
45	659.5	56.9	833	2	AAR24464	Aar24464 drosophil

ALIGNMENTS

RESULT 1
DLl1_HUMAN

```
ID   DLl1_HUMAN    STANDARD;    PRT;    723 AA.
AC   O00548; Q9NU41; Q9USV2;
DT   15-JUL-1998 (Rel. 36, Created)
DT   15-JUL-1998 (Rel. 36, Last sequence update)
DT   05-JUL-2004 (Rel. 44, Last annotation update)
DE   Delta-like protein 1 precursor (Drosophila Delta homolog 1) (Delta1)
DE   (H-Delta-1) (UNQ146/PRO172).
GN   Name=DLL1;
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Han W., Ye Q., Moore M.A.S.;
RT   "A soluble form of human delta-like-1 inhibits differentiation of
RT   hematopoietic progenitor cells.";
RL   Submitted (OCT-1999) to the EMBL/GenBank/DDBJ databases.
RN   [2]
RP   SEQUENCE FROM N.A.
RA   Gray G.E., Mann R.S., Mitsiadis E., Henrique D., Carcangiu M.-L.,
RA   Banks A., Leiman J., Ward D., Ish-Horowitz D., Artavanis-Tsakonas S.;
RT   "Human ligands of the Notch receptor.";
RL   Am. J. Pathol. 154:785-794(1999).
RN   [3]
RP   SEQUENCE FROM N.A.
RA   Oda T., Chandrasekharappa S.C.;
RT   "Human Delta 1 gene sequence.";
RL   Submitted (JAN-2000) to the EMBL/GenBank/DDBJ databases.
RN   [4]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=22872296; PubMed=12975309; DOI=10.1101/gr.1293003;
RA   Clark H.F., Gurney A.L., Abaya E., Baker K., Baldwin D., Brush J.,
RA   Chen J., Chow B., Chui C., Crowley C., Currell B., Deuel B., Dowd P.,
RA   Eaton D., Foster J., Grimaldi C., Gu Q., Hass P.E., Heldens S.,
RA   Huang A., Kim H.S., Klimowski L., Jin Y., Johnson S., Lee J.,
RA   Lewis L., Liao D., Mark M., Robbie E., Sanchez C., Schoenfeld J.,
RA   Seshagiri S., Simmons L., Singh J., Smith V., Stinson J., Vagts A.,
RA   Vandlen R., Watanabe C., Wieand D., Woods K., Xie M.-H., Yansura D.,
RA   Yi S., Yu G., Yuan J., Zhang M., Zhang Z., Goddard A., Wood W.I.,
RA   Godowski P.;
RT   "The secreted protein discovery initiative (SPDI), a large-scale
RT   effort to identify novel human secreted and transmembrane proteins: a
RT   bioinformatics assessment.";
RL   Genome Res. 13:2265-2270(2003).
RN   [5]
RP   SEQUENCE FROM N.A.
RA   Almeida J.;
RL   Submitted (APR-2000) to the EMBL/GenBank/DDBJ databases.
RN   [6]
RP   FUNCTION.
```

```
RX   MEDLINE=21464863; PubMed=11581320;
RA   Jaleco A.C., Neves H., Hooijberg E., Gameiro P., Clode N., Haury M.,
RA   Henrique D., Parreira L.;
RT   "Differential effects of Notch ligands Delta-1 and Jagged-1 in human
RT   lymphoid differentiation.";
RL   J. Exp. Med. 194:991-1001(2001).

CC   -!- FUNCTION: Acts as a ligand for Notch receptors. Blocks the
CC       differentiation of progenitor cells into the B-cell lineage while
CC       promoting the emergence of a population of cells with the
CC       characteristics of a T-cell/NK-cell precursor.
CC   -!- SUBUNIT: Interacts with Notch receptors.
CC   -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC   -!- TISSUE SPECIFICITY: Expressed in heart and pancreas, with lower
CC       expression in brain and muscle and almost no expression in
CC       placenta, lung, liver and kidney.
CC   -!- SIMILARITY: Contains 1 DSL domain.
CC   -!- SIMILARITY: Contains 8 EGF-like domains.
CC   -----------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   -----------------------------------------------------------------------

DR   EMBL; AF003522; AAB61286.1; -.
DR   EMBL; AF196571; AAF05834.1; -.
DR   EMBL; AF222310; AAG09716.1; -.
DR   EMBL; AY358892; AAQ89251.1; -.
DR   EMBL; AL078605; CAB89569.1; -.
DR   Genew; HGNC:2908; DLL1.
DR   MIM; 606582; -.
DR   HSSP; P00740; 1EDM.
DR   GO; GO:0005576; C:extracellular; NAS.
DR   GO; GO:0005887; C:integral to plasma membrane; NAS.
DR   GO; GO:0005112; F:Notch binding; IPI.
DR   GO; GO:0030154; P:cell differentiation; NAS.
DR   GO; GO:0001709; P:cell fate determination; NAS.
DR   GO; GO:0001701; P:embryonic development (sensu Mammalia); ISS.
DR   GO; GO:0009912; P:hair cell fate commitment; ISS.
DR   GO; GO:0030097; P:hemopoiesis; NAS.
DR   GO; GO:0042472; P:inner ear morphogenesis; ISS.
DR   GO; GO:0007399; P:neurogenesis; ISS.
DR   GO; GO:0007219; P:Notch signaling pathway; NAS.
DR   GO; GO:0042475; P:odontogenesis (sensu Vertebrata); ISS.
DR   GO; GO:0030155; P:regulation of cell adhesion; TAS.
DR   InterPro; IPR000152; DSL.
DR   InterPro; IPR001774; DSL.
DR   InterPro; IPR000742; EGF_2.
DR   InterPro; IPR001881; EGF_Ca.
DR   InterPro; IPR001438; EGF_II.
DR   InterPro; IPR006209; EGF.
DR   Pfam; PF01414; DSL; 1.
DR   Pfam; PF00008; EGF; 6.
DR   PRINTS; PR00010; EGFBLOOD.
DR   SMART; SM00051; DSL; 1.
DR   SMART; SM00179; EGF_CA; 4.
DR   PROSITE; PS00010; ASX_HYDROXYL; 3.
DR   PROSITE; PS00022; EGF_1; 8.
DR   PROSITE; PS01186; EGF_2; 8.
DR   PROSITE; PS50026; EGF_3; 7.
DR   PROSITE; PS01187; EGF_CA; 1.
DR   PROSITE; PS50027; DSL; 1.

KW   Developmental protein; Differentiation; EGF-like domain; Glycoprotein;
KW   Repeat; Signal; Transmembrane.
FT   SIGNAL        1     17       Potential.
FT   CHAIN        18    723       Delta-like protein 1.
FT   DOMAIN       18    545       Extracellular (Potential).
FT   TRANSMEM    546    568       Potential.
FT   DOMAIN      569    723       Cytoplasmic (Potential).
FT   DOMAIN      159    221       DSL.
FT   DOMAIN      226    254       EGF-like 1.
FT   DOMAIN      257    285       EGF-like 2.
FT   DOMAIN      292    325       EGF-like 3.
FT   DOMAIN      332    363       EGF-like 4; calcium-binding (Potential).
FT   DOMAIN      370    402       EGF-like 5.
FT   DOMAIN      409    440       EGF-like 6.
FT   DOMAIN      447    478       EGF-like 7; calcium-binding (Potential).
FT   DOMAIN      485    516       EGF-like 8.
FT   DISULFID    226    237       By similarity.
FT   DISULFID    230    243       By similarity.
FT   DISULFID    245    254       By similarity.
FT   DISULFID    257    268       By similarity.
FT   DISULFID    263    274       By similarity.
FT   DISULFID    276    285       By similarity.
FT   DISULFID    292    304       By similarity.
FT   DISULFID    298    314       By similarity.
FT   DISULFID    316    325       By similarity.
FT   DISULFID    332    343       By similarity.
FT   DISULFID    337    352       By similarity.
FT   DISULFID    354    363       By similarity.
FT   DISULFID    370    381       By similarity.
FT   DISULFID    375    391       By similarity.
FT   DISULFID    393    402       By similarity.
FT   DISULFID    409    420       By similarity.
FT   DISULFID    414    429       By similarity.
FT   DISULFID    431    440       By similarity.
FT   DISULFID    447    467       By similarity.
FT   DISULFID    469    478       By similarity.
FT   DISULFID    485    496       By similarity.
FT   DISULFID    490    505       By similarity.
FT   DISULFID    507    516       By similarity.
FT   CARBOHYD    477    477       N-linked (GlcNAc...) (Potential).
FT   CONFLICT    498    498       E -> Q (in Ref. 2).
FT   CONFLICT    502    502       G -> R (in Ref. 4 and 5).
FT   CONFLICT    510    510       G -> S (in Ref. 2).
SQ   SEQUENCE   723 AA;  77956 MW;  B4EC455FFA32A12B CRC64;

Query Match             100.0%;  Score 1160;  DB 1;  Length 723;
Best Local Similarity   100.0%;  Pred. No. 3.5e-88;
Matches  192;  Conservative   0;  Mismatches   0;  Indels   0;  Gaps   0;

Qy          1 GFTWPGTFSLIIEALHTDSPDDLATENPERLISRLATQRHLTVGEEWSQDLHSSGRTDLK 60
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        113 GFTWPGTFSLIIEALHTDSPDDLATENPERLISRLATQRHLTVGEEWSQDLHSSGRTDLK 172

Qy         61 YSYRFVCDEHYYGEGCSVFCRPRDDAFGHFTCGERGEKVCNPGWKGPYCTEPICLPGCDE 120
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        173 YSYRFVCDEHYYGEGCSVFCRPRDDAFGHFTCGERGEKVCNPGWKGPYCTEPICLPGCDE 232

Qy        121 QHGFCDKPGECKCRVGWQGRYCDECIRYPGCLHGTCQQPWQCNCQEGWGGLFCNQDLNYC 180
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        233 QHGFCDKPGECKCRVGWQGRYCDECIRYPGCLHGTCQQPWQCNCQEGWGGLFCNQDLNYC 292

Qy        181 THHKPCKNGATC 192
              ||||||||||||
Db        293 THHKPCKNGATC 304

RESULT 2
Q90656
ID   Q90656     PRELIMINARY;     PRT;   728 AA.
AC   Q90656;
DT   01-NOV-1996 (TrEMBLrel. 01, Created)
DT   01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   C-Delta-1.
OS   Gallus gallus (Chicken).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC   Gallus.
OX   NCBI_TaxID=9031;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Spinal cord;
RX   MEDLINE=95319507; PubMed=7596411;
```

OM protein - protein search, using sw model

GenCore version 5.1.6
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Run on: November 20, 2004, 16:28:50 ; Search time 22 Seconds
(without alignments)
839.710 Million cell updates/sec

Title: US-09-783-931-65
Perfect Score: 1160
Sequence: 1 GFTWPGTFSLIIEALHTDSP.........CNQDLNYCTHHKPCKNGATC 192
Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR.79:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1138	98.1	728	2	I50719	C-Delta-1 - chicke
2	1122	96.7	722	2	I48324	DELTA-like 1 - mou
3	709.5	61.2	685	2	JC7570	Delta-4 protein -
4	680.5	58.7	686	2	JC7569	Delta-4 protein -
5	659.5	56.9	832	2	A31246	neurogenic protein
6	659.5	56.9	833	2	S19087	gene Delta protein
7	659.5	56.9	880	2	S00670	neurogenic repetit
8	587	50.6	1220	2	A56136	jagged protein pre
9	533	45.6	1408	2	S16148	gene serrate prote
10	299.5	25.8	513	2	D88991	protein apx-1 [imp
11	288.5	24.9	385	2	S53718	homeotic protein d
12	280.5	24.2	385	2	A54785	preadipocyte facto
13	272.5	23.5	383	2	JC7125	epidermal growth f
14	272.5	23.5	383	2	S53716	delta-like homeoti
15	259	19.4	259	2	T21011	hypothetical prote
16	223.5	19.3	782	2	A61625	tenascin-like prot
17	211.5	18.2	3191	2	T22945	hypothetical prote
18	210.5	18.1	379	2	A59180	Wnt inhibitory fac
19	207	17.8	2471	2	A49128	cell-fate determin
20	205	17.7	1203	2	A49175	Notch B protein -
21	203.5	17.5	1111	2	T26972	hypothetical prote
22	197	17.0	2406	2	A54148	odz protein - frui
23	197	16.9	2515	2	D87900	tenascin-like prot
24	196	16.9	2318	2	S47008	notch 3 protein -
25	195	16.8	2321	2	S78549	notch3 protein - h
26	193	16.6	2019	1	JQ1322	tenascin precursor
27	193	16.6	2524	2	A35844	xotch protein - Af
28	190.5	16.4	1429	2	S06434	homeotic protein 1
29	188	16.2	1295	2	A32901	g1p1 protein precu
30	187.5	16.2	2825	2	T14271	Doc4 protein, stre
31	185.5	16.0	2555	2	A40043	notch protein homo
32	185	15.9	1746	1	S19694	tenascin precursor
33	184.5	15.9	378	2	B59180	Wnt inhibitory fac
34	184.5	15.9	1964	2	T09059	notch4 - mouse
35	184	15.9	2531	2	A46019	notch-1 protein -
36	183	15.9	2437	2	S42612	transmembrane prot
37	182.5	15.7	2918	2	A54105	fibrillin-2 precur
38	181.5	15.6	1574	2	T13954	MEGF6 protein - ra
39	181.5	15.6	2531	2	S18188	notch homo
40	180.5	15.6	2139	2	A35672	crumbs protein - f
41	180.5	15.6	2703	1	A24420	notch protein - fr
42	180	15.6	2437	2	A56175	notch protein - fr
43	179.5	15.5	2352	2	T30201	adhesive plaque pr
44	178	15.3	2201	2	A32160	tenascin-C - human
45	177.5	15.3	861	2	A48825	Notch homolog Motc

ALIGNMENTS

RESULT 1
I50719
C-Delta-1 - chicken
C;Species: Gallus gallus (chicken)
C;Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 09-Jul-2004
C;Accession: I50719
R;Henrique, D.; Adam, J.; Myat, A.; Chitnis, A.; Lewis, J.; Ish-Horowicz, D.
Nature 375, 787-790, 1995
A;Title: Expression of a Delta homologue in prospective neurons in the chick.
A;Reference number: I50719; MUID:95315507; PMID:7596411
A;Accession: I50719
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-728 <HEN>
A;Cross-references: UNIPROT:Q90656; EMBL:U26590; NID:g882411; PIDN:AAC59689.1; PID:g882
A;Superfamily: delta-4 protein; EGP homology
A;Keywords: EGF homology <EGX1>
F;299-332/Domain: EGF homology <EGF1>
F;339-370/Domain: EGF homology <EGX2>
F;416-447/Domain: EGF homology <EGX2>
F;454-485/Domain: EGF homology <EGF>
F;492-523/Domain: EGF homology <EGF3>

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Query Match             98.1%;  Score 1138;  DB 2;  Length 728;
Best Local Similarity   97.9%;  Pred. No. 6.1e-79;
Matches  188;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy    1 GFTWPGTFSLIIEALHTDSPDDLATENPRRLISRLATQRHLTVGEBWSQODLHSSGRTDLK 60
         ||||||||||||||||||||||| |||| ||||||||||| ||||||||||||||||||||
Db  120 GFTWPGTFSLIIEALHTDSPDDLTTENPERLISRLATQRHLAVGEBWSQODLHSSGRTDLK 179

Qy   61 YSYRFVCDEHYYGEGCSVFCRPRDDAFGHFTCGERGEKVCNPGWKGPYCTEPICLPGCDB 120
         |||||||||||||| |||||||||| |||||||||| |||||||||| ||||||||||||
Db  180 YSYRFVCDEHYYGBGCSVFCRPRDDRFGHFTCGERGEBKVCNPGWKGQYCTEPICLPGCDE 239

Qy  121 QHGFCDKPGBCKCRVGWQGRYCDBCIRYPGCLHGTCQQPWQCNCQBGWGGLFCNQDLNYC 180
         |||||||| ||||||||||||| |||||||||||||||||||||||||||||||||||||
Db  240 QHGFCDKPGSECKCRVGWQGRYCDECIRYPGCLHGTCQQPWQCNCQBGWGGLFCNQDLNYC 299

Qy  181 THHKPCKNGATC 192
         ||||||||||||
Db  300 THHKPCKNGATC 311
```

RESULT 2
I48324
DELTA-like 1 - mouse
C;Species: Mus musculus (house mouse)
C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 09-Jul-2004
C;Accession: I48324
R;Bettenhausen, B.; de Angelis, M.H.; Simon, D.; Guenet, J.L.; Gossler, A.
Development 121, 2407-2418, 1995
A;Title: Transient and restricted expression during mouse embryogenesis of Dll1, a muri

A;Reference number: 148324; MUID:95401858; PMID:7671806
A;Accession: 148324
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA <RES>
A;Residues: 1-722 <RES>
A;Cross-references: UNIPROT:Q61483; EMBL:X80903; NID:g8065569; PIDN:CAA55865.1; PID:g8065
A;Genetics:
A;Gene: Dll1
A;Superfamily: delta-4 protein; EGF homology
F;331-362/Domain: EGF homology <EGF2>
F;377-408/Domain: EGF homology <EGF>
F;484-477/Domain: EGF homology <EGF1>
F;484-515/Domain: EGF homology <EGF>

Query Match   96.7%;   Score 1122; DB 2;   Length 722;
Best Local Similarity 94.8%;   Pred. No. 9.8e-78;
Matches 182; Conservative 8; Mismatches 2; Indels 0; Gaps 0;

```
Qy     1 GFTWPGTFSLIIEALHTDSPDDLATENPERLISRLATQRHLTVGEEWSQDLHSSGRTDLK 60
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   112 GFTWPGTFSLIIEALHTDSPDDLATENPERLISRLTTQRHLTVGEEWSQDLHSSGRTDLR 171

Qy    61 YSYRFVCDEHYGEGCSVPCRPRDDAFGHPTCGERGEKVCNPGWKGPYCTEPICLPGCDB 120
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   172 YSYRFVCDEHYGBGCSVPCRPRDDAFGHPTCGDRGERWCMCDPGWKGQYCTDPICLPGCDD 231

Qy   121 QHGPCDKPGBCKCRVGWQGRYCDECIRYPGCLHGTCQOPWQCNCQEGWGGLFCNQDLNYC 180
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   232 QHGYCDKPGBCKCRVGWQGRYCDECIRYPGCLHGTCQQPWQCNCQBGWGGLFCNQDLNYC 291

Qy   181 THHKPCKNGATC 192
         ||||||||||||
Db   292 THHKPCRNGATC 303
```

RESULT 3
JC7570
Delta-4 protein - human
C;Species: Homo sapiens (man)
C;Date: 30-Jun-2001 #sequence_revision 30-Jun-2001 #text_change 09-Jul-2004
C;Accession: JC7570
R;Yoneya, T.; Tahara, T.; Nagao, K.; Yamada, Y.; Yamamoto, T.; Osawa, M.; Miyatani, S.;
J. Biochem. 129, 27-34, 2001
A;Title: Molecular cloning of Delta-4, a new mouse and human notch ligand.
A;Reference number: JC7569; MUID: 21064937; PMID:11134954
A;Accession: JC7570
A;Molecule type: mRNA
A;Superfamily: delta-4 protein; EGF homology
C;Keywords: transmembrane protein

Query Match   61.2%;   Score 709.5; DB 2;   Length 685;
Best Local Similarity 61.1%;   Pred. No. 1.7e-46;
Matches 118; Conservative 19; Mismatches 53; Indels 3; Gaps 2;

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Qy     2 FTWPGTFSLIIEALHTDSPDDLATE--NPERLISRLATQRHLTVGEEWSQDLHSSGRTDL 59
         ||||||||:|||:||:||||||||    :|||||||:||||||||||||:|||||||||:
Db   109 FTWPGTFSLIIBAWHAPG-DDLRPBALPPDALISKIALQGSLAVGQNMLLDEQTSTLTRL 167

Qy    60 KYSYRFVCDEHYGEGCSVPCRPRDDAFGHPTCGERGEKVCNPGWKGPYCTEPICLPGCD 119
         ||:|||:|||||:||||||||:||:|||||||||| |||:|||||||||:|||||||||
Db   168 RYSYRVICSDNYGDNCSRLCKRNDHPGHYVCQPDGNLSCLPGWTGBKYCQQPICLSGCH 227

Qy   120 EQHGPCDKPGBCKCRVGWQGRYCDECIRYPGCLHGTCQOPWQCNCQBGWGGLFCNQDLNY 179
         |:|:||||||||||||||||||||||||||||||||||||||||||||:||:||||||:
Db   228 BQNGYCSKPABCLCRPGWQGRLCNECIPHNGCRHGTCSTPWQCTCDEBGWGGLFCDQDLNY 287

Qy   180 CTHHKPCKNGATC 192
         ||||||||||||
Db   288 CTHHSPCKNGATC 300
```

RESULT 4
JC7569
Delta-4 protein - mouse
C;Species: Mus musculus (house mouse)
C;Date: 30-Jun-2001 #sequence_revision 30-Jun-2001 #text_change 09-Jul-2004
C;Accession: JC7569
R;Yoneya, T.; Tahara, T.; Nagao, K.; Yamada, Y.; Yamamoto, T.; Osawa, M.; Miyatani, S.;
A;Title: Molecular cloning of Delta-4, a new mouse and human notch ligand.
A;Reference number: JC7569; MUID: 21064937; PMID:11134954
A;Accession: JC7569
A;Molecule type: mRNA
A;Residues: 1-686 <YON>
A;Cross-references: UNIPROT:Q9DBU9; DDBJ:AB043893
C;Comment: This protein, a member of the Notch family of proteins, is a transmembrane r
ates the Notch signaling, the growth or differentiation of vascular endothelial cells.
C;Genetics:
A;Gene: delta-4
C;Superfamily: delta-4 protein; EGF homology

Query Match   58.7%;   Score 680.5; DB 2;   Length 686;
Best Local Similarity 59.6%;   Pred. No. 2.6e-44;
Matches 115; Conservative 17; Mismatches 58; Indels 3; Gaps 2;

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Qy     2 FTWPGTFSLINIQAWHTPG-DDLRPBTSPGNSLISQIIIQGSLAVGKIWRTDBQNDTLTRL 59
         ||||||||:|:|   |:|   :|||||||:||||||||||||:||||||||||||||||:
Db   110 FTWPGTFSLIIBALHTDSPDDLATENP--ERLISRLATQRHLTVGEEWSQDLHSSGRTDL 59

Qy    60 KYSYRFVCDEHYGEGCSVPCRPRDDAFGHPTCGERGEKVCNPGWKGPYCTEPICLPGCD 119
         ||:|||:|||||:||||||||:||:||||||||||:|||||||||||||||:|||||||
Db   169 SYSYRVICSDNYGBSCSRLCKRDDHFGHYBCQPDGSLSCLPGWTGKYCDQPICLSGCH 228

Qy   120 EQHGPCDKPGBCKCRVGWQGRYCDECIRYPGCLHGTCQOPWQCNCQBGWGGLFCNQDLNY 179
         |:|:||||||||||||||||||||||||||||||||||||||||||||:||:||||||:
Db   229 BQNGYCSKPDBCICRPGWQGRLCNECIPHNGCACDBGWGGLFCDQDLNY 288

Qy   180 CTHHKPCKNGATC 192
         ||||:|||||:||
Db   289 CTHHSPCKNGSTC 301
```

RESULT 5
A31246
neurogenic protein Delta precursor - fruit fly (Drosophila melanogaster)
C;Species: Drosophila melanogaster
C;Date: 31-Mar-1990 #sequence_revision 31-Mar-1990 #text_change 02-Aug-2002
C;Accession: A31246
R;Kopczynski, C.C.; Alton, A.K.; Fechtel, K.; Kooh, P.J.; Muskavitch, M.A.T.
Genes Dev. 2, 1723-1735, 1988
A;Title: Delta, a Drosophila neurogenic gene, is transcriptionally complex and encodes
A;Reference number: A31246; MUID:89196890; PMID:3149249
A;Accession: A31246
A;Molecule type: mRNA
A;Residues: 1-832 <KOP>
A;Cross-references: GB:Y00222
C;Genetics:
A;Gene: FlyBase:Dl
A;Cross-references: FlyBase:FBgn0000463
C;Superfamily: neurogenic protein delta; EGF homology
F;295-328/Domain: EGF homology <EGX1>
F;422-450/Domain: EGF homology <EGF>
F;457-488/Domain: EGF homology <EGF>
F;533-564/Domain: EGF homology <EGF3>

Query Match   56.9%;   Score 659.5; DB 2;   Length 832;
Best Local Similarity 56.0%;   Pred. No. 1.2e-42;
Matches 107; Conservative 25; Mismatches 56; Indels 3; Gaps 2;

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Qy     2 FTWPGTFSLIIEALHTDSPDDLATENPERLISRLATQRHLTVGEEWSQDLHSSGRTDLKY 61
         ||||||||:|||:||       ||||||||||||      |||||||||||:|||||||:
Db ...
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OM protein - protein search, using sw model

Copyright (c) 1993 - 2004 Compugen Ltd.
GenCore version 5.1.6

Run on: November 20, 2004, 16:36:05 ; Search time 69 seconds
(without alignments)
985.399 Million cell updates/sec

Title:
Perfect score: 1160
Sequence: US-09-783-931-65
1 GFTWPGTFSLIIBALHTDSP.........CNQDLNYCTHHKPCKNGATC 192

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1570615 seqs, 354127592 residues

Total number of hits satisfying chosen parameters: 1570615

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Database :   Published_Applications_AA:*
1: cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep:*
2: cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*
3: cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep:*
4: cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep:*
5: cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep:*
6: cgn2_6/ptodata/2/pubpaa/PCTUS_PUBCOMB.pep:*
7: cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep:*
8: cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep:*
9: cgn2_6/ptodata/2/pubpaa/US09A_PUBCOMB.pep:*
10: cgn2_6/ptodata/2/pubpaa/US09B_PUBCOMB.pep:*
11: cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep:*
12: cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep:*
13: cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pep:*
14: cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep:*
15: cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep:*
16: cgn2_6/ptodata/2/pubpaa/US10D_PUBCOMB.pep:*
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19: cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep:*
20: cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query % Match	Length	DB	ID	Description
1	1160	100.0	192	9	US-09-908-322-65	Sequence 65, Appl
2	1160	100.0	192	10	US-09-783-931-65	Sequence 65, Appl
3	1160	100.0	276	9	US-09-908-322-43	Sequence 43, Appl
4	1160	100.0	276	10	US-09-783-931-43	Sequence 43, Appl
5	1160	100.0	520	9	US-09-995-593A-3	Sequence 3, Appl
6	1160	100.0	702	9	US-09-995-593A-4	Sequence 4, Appl
7	1160	100.0	723	9	US-09-828-366-21	Sequence 21, Appl
8	1160	100.0	723	9	US-09-995-593A-9	Sequence 9, Appl
9	1160	100.0	723	14	US-10-028-072-346	Sequence 346, App
10	1160	100.0	723	14	US-10-140-808-346	Sequence 346, App
11	1160	100.0	723	14	US-10-121-049-346	Sequence 346, App
12	1160	100.0	723	14	US-11-123-904-346	Sequence 346, App
13	1160	100.0	723	14	US-10-140-470-346	Sequence 346, App
14	1160	100.0	723	14	US-10-175-746-346	Sequence 346, App
15	1160	100.0	723	14	US-10-176-918-346	Sequence 346, App
16	1160	100.0	723	14	US-10-176-921-346	Sequence 346, App
17	1160	100.0	723	14	US-10-137-865-346	Sequence 346, App
18	1160	100.0	723	14	US-10-140-474-346	Sequence 346, App
19	1160	100.0	723	14	US-10-142-431-346	Sequence 346, App
20	1160	100.0	723	14	US-10-143-1144-346	Sequence 346, App
21	1160	100.0	723	14	US-10-142-419-346	Sequence 346, App
22	1160	100.0	723	14	US-10-241-476-27	Sequence 27, Appl
23	1160	100.0	723	14	US-10-123-262-346	Sequence 346, App
24	1160	100.0	723	14	US-10-142-423-346	Sequence 346, App
25	1160	100.0	723	14	US-10-121-050-346	Sequence 346, App
26	1160	100.0	723	14	US-10-141-755-346	Sequence 346, App
27	1160	100.0	723	14	US-10-143-032-346	Sequence 346, App
28	1160	100.0	723	14	US-10-123-108-346	Sequence 346, App
29	1160	100.0	723	14	US-10-123-236-346	Sequence 346, App
30	1160	100.0	723	14	US-10-123-261-346	Sequence 346, App
31	1160	100.0	723	14	US-10-123-236-346	Sequence 346, App
32	1160	100.0	723	14	US-10-140-921-346	Sequence 346, App
33	1160	100.0	723	14	US-10-140-928-346	Sequence 346, App
34	1160	100.0	723	14	US-10-121-045-346	Sequence 346, App
35	1160	100.0	723	14	US-10-123-292-346	Sequence 346, App
36	1160	100.0	723	14	US-10-123-903-346	Sequence 346, App
37	1160	100.0	723	14	US-10-124-819-346	Sequence 346, App
38	1160	100.0	723	14	US-10-124-822-346	Sequence 346, App
39	1160	100.0	723	14	US-10-140-925-346	Sequence 346, App
40	1160	100.0	723	14	US-10-160-498-346	Sequence 346, App
41	1160	100.0	723	14	US-10-140-824-346	Sequence 346, App
42	1160	100.0	723	14	US-10-123-292-346	Sequence 346, App
43	1160	100.0	723	14	US-10-127-825A-346	Sequence 346, App
44	1160	100.0	723	14	US-10-127-829A-346	Sequence 346, App
45	1160	100.0	723	14	US-10-127-835A-346	Sequence 346, App
					US-10-127-839A-346	Sequence 346, App

ALIGNMENTS

RESULT 1
US-09-908-322-65
Sequence 65, Application US/09908322
Patent No. US20020107194A1
GENERAL INFORMATION:
APPLICANT: Ish-Horowicz, David
         Henrique, Domingos Manuel Pinto
         Lewis, Julian Hart
         Artavanis-Tsakonas, Spyridon
         Gray, Grace
TITLE OF INVENTION: NUCLEOTIDE AND PROTEIN SEQUENCES OF
         VERTEBRATE DELTA GENE AND METHODS BASED THEREON
NUMBER OF SEQUENCES: 94
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: NY
COUNTRY: USA
ZIP: 10036/2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/908,322
FILING DATE: 17-Jul-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/981,392
FILING DATE: 22-DEC-1997
ATTORNEY/AGENT INFORMATION:
NAME: Misrock, S Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 7326-123

```
                        TELECOMMUNICATION INFORMATION:
                          TELEPHONE: 212-790-9090
                          TELEX: 66141 PENNIE
                          TELEFAX: 212-869-8864

      INFORMATION FOR SEQ ID NO: 65:
        SEQUENCE CHARACTERISTICS:
          LENGTH: 192 amino acids
          TYPE: amino acid
          STRANDEDNESS: <Unknown>
          TOPOLOGY: unknown
        MOLECULE TYPE: peptide
        SEQUENCE DESCRIPTION: SEQ ID NO: 65:

US-09-908-322-65

Query Match       100.0%;  Score 1160;  DB 9;  Length 192;
Best Local Similarity  100.0%;  Pred. No. 2.2e-90;
Matches 192;  Conservative 0;  Mismatches 0;  Indels 0;  Gaps 0;

Qy   1 GFTWPGTFSLIIBALHTDSPDDLATENPERLISRLATQRHLTVGBEWSQDLHSSGRTDLK 60
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Db   1 GFTWPGTFSLIIBALHTDSPDDLATENPERLISRLATQRHLTVGBEWSQDLHSSGRTDLK 60

Qy  61 YSYRFVCDEHYYGBGCSVFCRPRDDAFGHPTCGERGERKVCNPGWKGPYCTEPICLPGCDB 120
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  61 YSYRFVCDEHYYGBGCSVFCRPRDDAFGHPTCGERGERKVCNPGWKGPYCTEPICLPGCDB 120

Qy 121 QHGPCDKPGEBCKCRVGWQGRYCDECIRYPGCLHGTCQOPWQCNCQEBGWGGLFCNQDLNYC 180
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 121 QHGPCDKPGEBCKCRVGWQGRYCDECIRYPGCLHGTCQOPWQCNCQEBGWGGLFCNQDLNYC 180

Qy 181 THHKPCKNGATC 192
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Db 181 THHKPCKNGATC 192
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RESULT 2
US-09-783-931-65
Sequence 65, Application US/09783931
Publication No. US20030073620A1
GENERAL INFORMATION:
  APPLICANT: Ish-Horowicz, David
           Henrique, Domingos Manuel Pinto
           Lewis, Julian Hart
           Artavanis-Tsakonas, Spyridon
           Gray, Grace
  TITLE OF INVENTION: ANTIBODIES TO VERTEBRATE DELTA PROTEINS
                      AND FRAGMENTS
  NUMBER OF SEQUENCES: 94
  CORRESPONDENCE ADDRESS:
    ADDRESSEE: Pennie & Edmonds LLP
    STREET: 1155 Avenue of the Americas
    CITY: New York
    STATE: NY
    COUNTRY: USA
    ZIP: 10036/2711
  COMPUTER READABLE FORM:
    MEDIUM TYPE: Diskette
    COMPUTER: IBM Compatible
    OPERATING SYSTEM: DOS
    SOFTWARE: FastSEQ Version 2.0
  CURRENT APPLICATION DATA:
    APPLICATION NUMBER: US/09/783,931
    FILING DATE: 15-Feb-2001
    CLASSIFICATION: <Unknown>
  PRIOR APPLICATION DATA:
    APPLICATION NUMBER: 08/981,392
    FILING DATE: 22-DEC-1997
  ATTORNEY/AGENT INFORMATION:
    NAME: Antler, Adriane M.
    REGISTRATION NUMBER: 32,605
    REFERENCE/DOCKET NUMBER: 7326-122
  TELECOMMUNICATION INFORMATION:
    TELEPHONE: 212-790-9090

```
                          TELEFAX: 212-869-8864
                          TELEX: 66141 PENNIE

      INFORMATION FOR SEQ ID NO: 65:
        SEQUENCE CHARACTERISTICS:
          LENGTH: 192 amino acids
          TYPE: amino acid
          STRANDEDNESS: <Unknown>
          TOPOLOGY: unknown
        MOLECULE TYPE: peptide
        SEQUENCE DESCRIPTION: SEQ ID NO: 65:

US-09-783-931-65

Query Match       100.0%;  Score 1160;  DB 10;  Length 192;
Best Local Similarity  100.0%;  Pred. No. 2.2e-90;
Matches 192;  Conservative 0;  Mismatches 0;  Indels 0;  Gaps 0;

Qy   1 GFTWPGTFSLIIBALHTDSPDDLATENPERLISRLATQRHLTVGBEWSQDLHSSGRTDLK 60
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Db   1 GFTWPGTFSLIIBALHTDSPDDLATENPERLISRLATQRHLTVGBEWSQDLHSSGRTDLK 60

Qy  61 YSYRFVCDEHYYGBGCSVFCRPRDDAFGHPTCGERGERKVCNPGWKGPYCTEPICLPGCDB 120
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Qy 121 QHGPCDKPGEBCKCRVGWQGRYCDECIRYPGCLHGTCQOPWQCNCQEBGWGGLFCNQDLNYC 180
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Db 121 QHGPCDKPGEBCKCRVGWQGRYCDECIRYPGCLHGTCQOPWQCNCQEBGWGGLFCNQDLNYC 180

Qy 181 THHKPCKNGATC 192
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Db 181 THHKPCKNGATC 192
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RESULT 3
US-09-908-322-43
Sequence 43, Application US/09908322
Patent No. US20020107194A1
GENERAL INFORMATION:
  APPLICANT: Ish-Horowicz, David
           Henrique, Domingos Manuel Pinto
           Lewis, Julian Hart
           Artavanis-Tsakonas, Spyridon
           Gray, Grace
  TITLE OF INVENTION: NUCLEOTIDE AND PROTEIN SEQUENCES OF
                      VERTEBRATE DELTA GENE AND METHODS BASED THEREON
  NUMBER OF SEQUENCES: 94
  CORRESPONDENCE ADDRESS:
    ADDRESSEE: Pennie & Edmonds LLP
    STREET: 1155 Avenue of the Americas
    CITY: New York
    STATE: NY
    COUNTRY: USA
    ZIP: 10036/2711
  COMPUTER READABLE FORM:
    MEDIUM TYPE: Diskette
    COMPUTER: IBM Compatible
    OPERATING SYSTEM: DOS
    SOFTWARE: FastSEQ Version 2.0
  CURRENT APPLICATION DATA:
    APPLICATION NUMBER: US/09/908,322
    FILING DATE: 17-Jul-2001
    CLASSIFICATION: <Unknown>
  PRIOR APPLICATION DATA:
    APPLICATION NUMBER: 08/981,392
    FILING DATE: 22-DEC-1997
  ATTORNEY/AGENT INFORMATION:
    NAME: Misrock, S Leslie
    REGISTRATION NUMBER: 18,872
    REFERENCE/DOCKET NUMBER: 7326-123
  TELECOMMUNICATION INFORMATION:
    TELEPHONE: 212-790-9090
    TELEFAX: 212-869-8864
    TELEX: 66141 PENNIE

OM protein - protein search, using sw model

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1993 - 2004 Compugen Ltd.

Run on: November 20, 2004, 15:47:05 ; Search time 23 seconds
                 (without alignments)
                 553.611 Million cell updates/sec

Title: US-09-783-931-65
Perfect score: 1160
Sequence: 1 GFTWPGTFSLIIEALHTDSP..........CNQDLNYCTHHKPCKNGATC 192

Scoring table: BLOSUM62
                 Gapop 10.0 , Gapext 0.5

Searched: 478139 seqs, 66318000 residues

Total number of hits satisfying chosen parameters: 478139

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Database :   Issued_Patents_AA:*
                 1: /cgn2_6/ptcdata/1/iaa/5A_COMB.pep:*
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                 3: /cgn2_6/ptcdata/1/iaa/6A_COMB.pep:*
                 4: /cgn2_6/ptcdata/1/iaa/6B_COMB.pep:*
                 5: /cgn2_6/ptcdata/1/iaa/PCTUS_COMB.pep:*
                 6: /cgn2_6/ptcdata/1/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1160	100.0	192	3	US-08-981-392-65	Sequence 65, Appl
2	1160	100.0	192	4	US-09-908-322-65	Sequence 65, Appl
3	1160	100.0	276	3	US-08-981-39-43	Sequence 43, Appl
4	1160	100.0	276	4	US-09-908-322-43	Sequence 43, Appl
5	1160	100.0	520	4	US-09-068-740A-3	Sequence 3, Appl
6	1160	100.0	702	3	US-09-068-740A-4	Sequence 4, Appl
7	1160	100.0	723	3	US-09-068-740A-9	Sequence 9, Appl
8	1160	100.0	723	4	US-09-423-753-27	Sequence 27, Appl
9	1160	100.0	723	4	US-10-140-000-346	Sequence 346, App
10	1153	99.4	723	4	US-09-641-612-6	Sequence 6, Appl
11	1138	98.1	728	4	US-08-981-392-2	Sequence 2, Appl
12	1138	98.1	728	4	US-09-908-322-2	Sequence 2, Appl
13	1138	98.1	729	3	US-08-872-855-8	Sequence 8, Appl
14	1119	96.5	722	4	US-08-981-392-12	Sequence 12, Appl
15	1119	96.5	722	4	US-08-872-855-12	Sequence 12, Appl
16	1110.5	95.7	713	3	US-08-872-855-4	Sequence 4, Appl
17	1107.5	95.5	720	3	US-08-872-855-5	Sequence 5, Appl
18	1077	92.8	721	4	US-09-908-322-5	Sequence 5, Appl
19	1077	92.8	721	3	US-08-981-392-5	Sequence 5, Appl
20	1072	92.4	721	4	US-09-908-322-5	Sequence 5, Appl
21	1059	91.3	717	3	US-08-872-855-7	Sequence 7, Appl
22	965	83.2	578	4	US-08-981-392-13	Sequence 13, Appl
23	965	83.2	578	3	US-09-908-322-13	Sequence 13, Appl
24	835.5	72.0	642	3	US-08-872-855-10	Sequence 10, Appl
25	709.5	61.2	500	4	US-09-423-753-2	Sequence 2, Appl
26	709.5	61.2	659	4	US-09-423-753-3	Sequence 3, Appl
27	709.5	61.2	685	3	US-08-872-855-2	Sequence 2, Appl
28	709.5	61.2	685	4	US-09-423-753-25	Sequence 25, Appl
29	709.5	61.2	685	4	US-09-641-612-7	Sequence 7, Appl
30	709.5	61.2	685	4	US-10-140-002-88	Sequence 88, Appl
31	709.5	56.9	830	3	US-08-872-855-11	Sequence 11, Appl
32	659.5	56.9	832	3	US-08-981-392-6	Sequence 6, Appl
33	659.5	56.9	832	4	US-09-908-322-6	Sequence 6, Appl
34	659.5	51.4	1193	2	US-08-264-534-6	Sequence 6, Appl
35	659.5	56.9	833	1	US-09-068-740A-2	Sequence 2, Appl
36	659.5	56.9	833	2	US-08-083-590A-2	Sequence 2, Appl
37	659.5	56.9	833	2	US-08-465-500-6	Sequence 6, Appl
38	659.5	56.9	833	2	US-08-346-128-6	Sequence 6, Appl
39	659.5	56.9	833	3	US-08-346-126-6	Sequence 6, Appl
40	659.5	52.7	833	3	US-08-532-384-2	Sequence 2, Appl
41	611	52.7	200	3	US-09-068-740A-2	Sequence 2, Appl
42	596	51.4	1193	2	US-08-400-159-10	Sequence 10, Appl
43	596	51.4	1193	4	US-08-611-729A-10	Sequence 10, Appl
44	596	51.4	1193	4	US-08-195-524-10	Sequence 10, Appl
45	591.5	51.0	1055	3	US-09-214-278-2	Sequence 2, Appl

ALIGNMENTS

RESULT 1
US-08-981-392-65
; Sequence 65, Application US/08981392
; Patent No. 6262025
; GENERAL INFORMATION:
; APPLICANT: Ish-Horowicz, David
; APPLICANT: Henrique, Domingos Manuel Pinto
; APPLICANT: Lewis, Julian Hart
; APPLICANT: Artavanis-Tsakonas, Spyridon
; APPLICANT: Gray, Grace
; TITLE OF INVENTION: NUCLEOTIDE AND PROTEIN SEQUENCES
; TITLE OF INVENTION: OF VERTEBRATE DELTA GENES AND METHODS BASED THEREON
; NUMBER OF SEQUENCES: 94
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10036/2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/981,392
; FILING DATE: 22-DEC-1997
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Antler, Adriane M.
; REGISTRATION NUMBER: 32,605
; REFERENCE/DOCKET NUMBER: 7326-038
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-790-9090
; TELEFAX: 212-869-8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 65:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 192 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
US-08-981-392-65

Query Match   100.0%; Score 1160; DB 3; Length 192;
Best Local Similarity   100.0%; Pred. No. 4.1e-92;
Matches 192; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

```
Qy    1 GFTWPGTFSLIIEALHTDSPDDLATENPERLISRLATQRHLTVGEEWSQDLHSSGRTDLK 60
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1 GFTWPGTFSLIIEALHTDSPDDLATENPERLISRLATQRHLTVGEEWSQDLHSSGRTDLK 60

Qy   61 YSYRFVCDEHYYGEGCSVFCRPRDDAFGHFTCGERGEKVCNPGWKGPYCTEPICLPGCDE 120
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 YSYRFVCDEHYYGEGCSVFCRPRDDAFGHFTCGERGEKVCNPGWKGPYCTEPICLPGCDE 120

Qy  121 QHGFCDKPGECKCRVGWQGRYCDECIRYPGCLHGTCQQPWQCNCQEGWGGLFCNQDLNYC 180
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  121 QHGFCDKPGECKCRVGWQGRYCDECIRYPGCLHGTCQQPWQCNCQEGWGGLFCNQDLNYC 180

Qy  181 THHKPCKNGATC 192
        ||||||||||||
Db  181 THHKPCKNGATC 192
```

RESULT 2
US-09-908-322-65
; Sequence 65, Application US/09908322
; Patent No. 6783956
GENERAL INFORMATION:
APPLICANT: Ish-Horowicz, David
APPLICANT: Henrique, Domingos Manuel Pinto
APPLICANT: Lewis, Julian Hart
APPLICANT: Artavanis-Tsakonas, Spyridon
APPLICANT: Gray, Grace
TITLE OF INVENTION: NUCLEOTIDE AND PROTEIN SEQUENCES OF VERTEBRATE DELTA GENE AND METHODS BASED THEREON
NUMBER OF SEQUENCES: 94
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: NY
COUNTRY: USA
ZIP: 10036/2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/908,322
FILING DATE: 17-Jul-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/981,392
FILING DATE: 22-DEC-1997
ATTORNEY/AGENT INFORMATION:
NAME: Misrock, S Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 7326-123
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-790-9090
TELEFAX: 212-869-8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 65:
SEQUENCE CHARACTERISTICS:
LENGTH: 192 amino acid
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: unknown
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 65:
US-09-908-322-65

Query Match 100.0%; Score 1160; DB 4; Length 192;
Best Local Similarity 100.0%; Pred. No. 4.1e-92;
Matches 192; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy    1 GFTWPGTFSLIIEALHTDSPDDLATENPERLISRLATQRHLTVGEEWSQDLHSSGRTDLK 60
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
```

```
Db    1 GFTWPGTFSLIIEALHTDSPDDLATENPERLISRLATQRHLTVGEEWSQDLHSSGRTDLK 60

Qy   61 YSYRFVCDEHYYGEGCSVFCRPRDDAFGHFTCGERGEKVCNPGWKGPYCTEPICLPGCDE 120
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 YSYRFVCDEHYYGEGCSVFCRPRDDAFGHFTCGERGEKVCNPGWKGPYCTEPICLPGCDE 120

Qy  121 QHGFCDKPGECKCRVGWQGRYCDECIRYPGCLHGTCQQPWQCNCQEGWGGLFCNQDLNYC 180
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  121 QHGFCDKPGECKCRVGWQGRYCDECIRYPGCLHGTCQQPWQCNCQEGWGGLFCNQDLNYC 180

Qy  181 THHKPCKNGATC 192
        ||||||||||||
Db  181 THHKPCKNGATC 192
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RESULT 3
US-08-981-392-43
; Sequence 43, Application US/08981392
; Patent No. 6262025
GENERAL INFORMATION:
APPLICANT: Ish-Horowicz, David
APPLICANT: Henrique, Domingos Manuel Pinto
APPLICANT: Lewis, Julian Hart
APPLICANT: Artavanis-Tsakonas, Spyridon
APPLICANT: Gray, Grace
TITLE OF INVENTION: NUCLEOTIDE AND PROTEIN SEQUENCES
TITLE OF INVENTION: OF VERTEBRATE DELTA GENES AND METHODS BASED THEREON
NUMBER OF SEQUENCES: 94
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: NY
COUNTRY: USA
ZIP: 10036/2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/981,392
FILING DATE: 22-DEC-1997
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Antler, Adriane M.
REGISTRATION NUMBER: 32,605
REFERENCE/DOCKET NUMBER: 7326-038
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-790-9090
TELEFAX: 212-869-8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 43:
SEQUENCE CHARACTERISTICS:
LENGTH: 276 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY:
MOLECULE TYPE: peptide
US-08-981-392-43

Query Match 100.0%; Score 1160; DB 3; Length 276;
Best Local Similarity 100.0%; Pred. No. 6.1e-92;
Matches 192; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy    1 GFTWPGTFSLIIEALHTDSPDDLATENPERLISRLATQRHLTVGEEWSQDLHSSGRTDLK 60
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   20 GFTWPGTFSLIIEALHTDSPDDLATENPERLISRLATQRHLTVGEEWSQDLHSSGRTDLK 79

Qy   61 YSYRFVCDEHYYGEGCSVFCRPRDDAFGHFTCGERGEKVCNPGWKGPYCTEPICLPGCDE 120
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   80 YSYRFVCDEHYYGEGCSVFCRPRDDAFGHFTCGERGEKVCNPGWKGPYCTEPICLPGCDE 139
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OM protein - protein search, using sw model

GenCore version 5.1.6
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Run on: November 20, 2004, 15:43:51 ; Search time 74 Seconds
(without alignments)
930.757 Million cell updates/sec

Title: US-09-783-931-65
Perfect score: 1160
Sequence: 1 GFTWPGTFSLIIEALHTDSP..........CNQDLNYCTHHKPCKNGATC 192
Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5
Searched: 2002273 seqs, 358729299 residues

Total number of hits satisfying chosen parameters: 2002273

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :   A_Geneseq_23Sep04:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1160	100.0	192	2	AAW11728	Aaw11728 H-Delta-1
2	1160	100.0	331	6	ABR61806	Abr61806 Human DLL
3	1160	100.0	331	7	ABR61735	Abr61735 Human DLL
4	1160	100.0	331	8	ADJ45785	Adj45785 Delta1 (D
5	1160	100.0	332	8	ABU63727	Abu63727 Notch lig
6	1160	100.0	332	8	ADJ45799	Adj45799 D1B3Cys P
7	1160	100.0	332	8	ADJ73006	Adj73006 Human Not
8	1160	100.0	332	8	ADM75990	Adm75990 Human del
9	1160	100.0	369	7	ABR61807	Abr61807 Human DLL
10	1160	100.0	369	7	ABR61736	Abr61736 Human DLL
11	1160	100.0	369	8	ADJ45790	Adj45790 Delta1 (D
12	1160	100.0	369	8	ADL72998	Adl72998 Human Not
13	1160	100.0	369	6	ABR61808	Abr61808 Human DLL
14	1160	100.0	484	7	ABR61737	Abr61737 Human DLL
15	1160	100.0	484	8	ADJ45795	Adj45795 Delta1 (D
16	1160	100.0	484	8	ADL72986	Adl72986 Human Not
17	1160	100.0	512	2	AAW75494	Aaw75494 Truncated
18	1160	100.0	520	8	AAW18348	Aaw18348 Prolifera
19	1160	100.0	520	8	ADK67909	Adk67909 Human ext
20	1160	100.0	660	2	AAW11726	Aaw11726 H-Delta-1
21	1160	100.0	702	2	AAW18349	Aaw18349 Prolifera
22	1160	100.0	702	2	AAW75495	Aaw75495 Truncated
23	1160	100.0	723	2	AAW18353	Aaw18353 Prolifera
24	1160	100.0	723	2	AAW75492	Aaw75492 Human del
25	1160	100.0	723	2	AAW94498	Aaw94498 Human del
26	1160	100.0	723	3	AAY83227	Aay83227 PRO172 Po
27	1160	100.0	723	3	AAB33422	Aab33422 Human PRO
28	1160	100.0	723	3	AAB24388	Aab24388 Human PRO
29	1160	100.0	723	3	AAY79032	Aay79032 Human del
30	1160	100.0	723	3	AAB00172	Aab00172 PRO172 Po
31	1160	100.0	723	4	AAU12344	Aau12344 Human PRO
32	1160	100.0	723	4	AAB53064	Aab53064 Human ang
33	1160	100.0	723	6	ABO17788	Abo17788 Novel hum
34	1160	100.0	723	6	ABU81042	Abu81042 Human PRO
35	1160	100.0	723	6	ABP97824	Abp97824 Human PRO
36	1160	100.0	723	6	ABU66742	Abu66742 Amino aci
37	1160	100.0	723	6	ABU55879	Abu55879 Human not
38	1160	100.0	723	6	AAE34035	Aae34035 Novel sec
39	1160	100.0	723	6	ABU59823	Abu59823 Novel sec
40	1160	100.0	723	6	ABO25013	Abo25013 Human sec
41	1160	100.0	723	6	ABP72566	Abp72566 Human Not
42	1160	100.0	723	6	ABU67018	Abu67018 Human sec
43	1160	100.0	723	6	ADA45865	Ada45865 Novel hum
44	1160	100.0	723	6	ADA76296	Ada76296 Human PRO
45	1160	100.0	723	6	ADA18946	Ada18946 Human PRO

ALIGNMENTS

RESULT 1
ID   AAW11728
AAW11728 AAW11728 standard; protein; 192 AA.
XX
AC   AAW11728;
XX
DT   28-APR-1997 (first entry)
XX
DE   H-Delta-1 polypeptide (aa 1-192).
XX
KW   H-Delta-1; cell proliferation; nervous system disorder;
KW   tissue regeneration; Notch; cervix cancer; breast cancer; lung cancer;
KW   colon cancer; melanoma; seminoma; neurogenesis; therapy.
XX
OS   Homo sapiens.
XX
FH
PN   WO9701571-A1.
XX
PD   16-JAN-1997.
XX
PF   28-JUN-1996; 96WO-US011178.
XX
PR   28-JUN-1995; 95US-0000589P.
XX
PA   (IMCR) IMPERIAL CANCER RES TECHNOLOGY.
PA   (UYVA) UNIV YALE.
XX
PI   Ish-Horowicz D, Henrique D, Lewis J, Artavanis-Tsakonas S;
PI   Gray GR;
XX
PT   New vertebrate Delta protein, DNA and antibodies - for treating and
PT   preventing cancer, nervous system disorders and for tissue regeneration.
XX
PR   WPI; 1997-100159/09.
XX
PS   Claim 84; Fig 14A; 135pp; English.
XX
CC   Human Delta-1 includes the polypeptide sequences given in AAW11728-38.
CC   Amino acid residues 1-192 are given in AAW11728. The polypeptides were
CC   identified from the translation products (see also AAW11725-27) of a H-
CC   Delta-1 contig (AAT59454) derived from a foetal brain library. Errors in
CC   the contig resulted in frameshifts, and the H-Delta-1 amino acid sequence
CC   had to be deduced from the 3 translated sequences by homology to chick
CC   and mouse Delta-1 (see also AAW11719-20). H-Delta-1 is a homologue of
CC   Drosophila Delta, a protein that binds to Notch. H-Delta-1 polypeptides
CC   can be used to treat disorders of cell fate or differentiation, such as
CC   cancer, and nervous system disorders, or to promote tissue regeneration
CC   and repair

XX
SQ   Sequence 192 AA;

     Query Match   100.0%; Score 1160; DB 2; Length 192;
     Best Local Similarity   100.0%; Pred. No. 2.3e-76;
     Matches 192; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Qy   1 GPTWPGTFSLIIEALHTDSPDDLATENPERLISRLATQRHLTVGEEWSQDLHSSGRTDLK 60
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Db   1 GPTWPGTFSLIIEALHTDSPDDLATENPERLISRLATQRHLTVGEEWSQDLHSSGRTDLK 60

Qy   61 YSYRFVCDEHYYGEGCSVPCRPRDDAFGHFTCGERGEKVCNPGWKGPYCTEPICLPGCDB 120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 YSYRFVCDEHYYGEGCSVPCRPRDDAFGHFTCGERGEKVCNPGWKGPYCTEPICLPGCDB 120

Qy   121 QHGFCDKPGEBCKCRVGWQGRYCDECIRYPGCLHGTCQQPWQCNCQEGWGGLFCNQDLNYC 180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   121 QHGFCDKPGEBCKCRVGWQGRYCDECIRYPGCLHGTCQQPWQCNCQEGWGGLFCNQDLNYC 180

Qy   181 THHKPCKNGATC 192
            ||||||||||||
Db   181 THHKPCKNGATC 192

RESULT 2
ID   ABR61806 standard; protein; 331 AA.
XX
AC   ABR61806;
XX
DT   23-OCT-2003   (revised)
DT   03-SEP-2003   (first entry)
XX
DE   Human DLL-1 EGF1-3-IgG4Fc fusion protein sequence.
XX
KW   Notch signaling; notch ligand; immunostimulant; antimicrobial; EGF;
KW   epidermal growth factor; medicament; vaccine; delta 1; DLL-1; IgG4Fc;
KW   fusion protein.
XX
OS   Homo sapiens.
OS   Chimeric.
XX
PN   WO2003041735-A2.
XX
PD   22-MAY-2003.
XX
PF   13-NOV-2002; 2002WO-GB005137.
XX
PR   14-NOV-2001; 2001GB-00027267.
PR   25-JUL-2002; 2002WO-GB003426.
PR   07-SEP-2002; 2002GB-00020849.
PR   10-SEP-2002; 2002GB-00020913.
PR   27-SEP-2002; 2002WO-GB004390.
XX
PA   (LORA-) LORANTIS LTD.
XX
PI   Bodmer MW, Briend ECP, Champion BR, Lennard AC, Mckenzie GJ;
PI   Ragno S, Tugal T, Young LL;
XX
DR   WPI; 2003-449535/42.
XX
PT   New product comprising a Notch signaling pathway inhibitor and a pathogen
PT   antigen or antigenic determinant, useful for stimulating the immune
PT   system to treat or prevent an infection, or for treating a chronic
PT   pathogen infection.
XX
PS   Example 21; Page 169-170; 256pp; English.
XX
CC   The invention relates to a product comprising an inhibitor of the Notch
CC   signaling pathway or a polynucleotide coding for such inhibitor; and a
CC   pathogen antigen or antigenic determinant, or a polynucleotide coding for
CC   such pathogen antigen or antigenic determinant, as a combined preparation
CC   for simultaneous, contemporaneous, separate or sequential use for
CC   modulating the immune system. The inhibitor of Notch signaling pathway is
CC   useful in the manufacture of a medicament for use as a stimulant, but not
CC   for reversing bacteria, infection, or tumor-induced immunosuppression, or
CC   for treating tumor. The inhibitor is also useful for stimulating the immune
CC   system to treat or prevent an infection in (enhancing) vaccination
CC   against a pathogen, treating a chronic pathogen infection, and in
CC   increasing the immune response of a subject to a vaccine antigen or
CC   antigenic determinant. The binding agent that binds to a Notch ligand, an
CC   antibody or its derivative that binds to a Notch receptor or Notch
CC   ligand, or the polynucleotide encoding these, may also be used in the
CC   manufacture of a medicament for use as a stimulant. The antibody or
CC   antibody derivative may further be used in stimulating the immune system.
CC   The present sequence represents a human delta 1 (DLL-1) EGF1-3 -IgG4Fc
CC   fusion protein. (Updated on 23-OCT-2003 to standardise OS field)
XX
SQ   Sequence 331 AA;

     Query Match   100.0%; Score 1160; DB 6; Length 331;
     Best Local Similarity   100.0%; Pred. No. 3.7e-76;
     Matches 192; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Qy   1 GPTWPGTFSLIIEALHTDSPDDLATENPERLISRLATQRHLTVGEEWSQDLHSSGRTDLK 60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   113 GPTWPGTFSLIIEALHTDSPDDLATENPERLISRLATQRHLTVGEEWSQDLHSSGRTDLK 172

Qy   61 YSYRFVCDEHYYGEGCSVPCRPRDDAFGHFTCGERGEKVCNPGWKGPYCTEPICLPGCDB 120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   173 YSYRFVCDEHYYGEGCSVPCRPRDDAFGHFTCGERGEKVCNPGWKGPYCTEPICLPGCDB 232

Qy   121 QHGFCDKPGEBCKCRVGWQGRYCDECIRYPGCLHGTCQQPWQCNCQEGWGGLFCNQDLNYC 180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   233 QHGFCDKPGEBCKCRVGWQGRYCDECIRYPGCLHGTCQQPWQCNCQEGWGGLFCNQDLNYC 292

Qy   181 THHKPCKNGATC 192
            ||||||||||||
Db   293 THHKPCKNGATC 304

RESULT 3
ID   ABR61735 standard; protein; 331 AA.
XX
AC   ABR61735;
XX
DT   23-OCT-2003   (revised)
DT   02-SEP-2003   (first entry)
XX
DE   Human DLL-1 EGF1-3-IgG4Fc fusion protein sequence.
XX
KW   Notch signaling; cancer; notch ligand; epidermal growth factor; EGF;
KW   cytostatic; vaccine; human; delta 1; DLL-1; IgG4Fc; fusion protein.
XX
OS   Homo sapiens.
OS   Chimeric.
XX
PN   WO2003042246-A2.
XX
PD   22-MAY-2003.
XX
PF   13-NOV-2002; 2002WO-GB005133.
XX
PR   14-NOV-2001; 2001GB-00027271.
PR   10-SEP-2002; 2002GB-00020913.
XX
PA   (LORA-) LORANTIS LTD.
XX
PI   Bodmer MW, Briend ECP, Champion BR, Lennard AC, Mckenzie GJ;
PI   Ragno S, Tugal T, Young LL;
XX
DR   WPI; 2003-449560/42.
XX
PT   New inhibitor of Notch signaling, useful for preventing or treating
PT   cancer e.g. breast, liver, kidney or colon cancer.

OM nucleic - nucleic search, using sw model

Run on: November 20, 2004, 15:36:12 ; Search time 431 Seconds
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                 GenCore version 5.1.6

Title: US-09-783-931-26_COPY_60_665
Perfect score: 606
Sequence: 1 GCTTCACCTGGCCGGGCACC..........GCCAGGGGGAGCTACACTTG 606

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Searched: 3627888 seqs, 2701811610 residues

Total number of hits satisfying chosen parameters: 7255776

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Database :   Published Applications NA:*
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                 8: /cgn2_6/ptodata/2/pubpna/US08_PUBCOMB.seq:*
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	605	99.8	1981	9	US-09-908-322-26	Sequence 26, Appl
2	605	99.8	1981	10	US-09-783-931-26	Sequence 26, Appl
3	579.8	95.7	2183	17	US-10-644-548-9	Sequence 9, Appli
4	579.8	95.7	2663	9	US-09-995-593A-8	Sequence 8, Appli
5	579.8	95.7	2663	14	US-10-241-476-8	Sequence 8, Appli
6	579.8	95.7	2933	9	US-09-828-366-20	Sequence 20, Appl
7	579.8	95.7	2933	14	US-10-028-072-345	Sequence 345, App
8	579.8	95.7	2933	14	US-10-140-808-345	Sequence 345, App
9	579.8	95.7	2933	14	US-10-121-049-345	Sequence 345, App
10	579.8	95.7	2933	14	US-10-123-904-345	Sequence 345, App
11	579.8	95.7	2933	14	US-10-140-470-345	Sequence 345, App
12	579.8	95.7	2933	14	US-10-175-746-345	Sequence 345, App
13	579.8	95.7	2933	14	US-10-176-918-345	Sequence 345, App
14	579.8	95.7	2933	14	US-10-176-921-345	Sequence 345, App
15	579.8	95.7	2933	14	US-10-137-865-345	Sequence 345, App
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17	579.8	95.7	2933	14	US-10-142-431-345	Sequence 345, App
18	579.8	95.7	2933	14	US-10-143-114-345	Sequence 345, App
19	579.8	95.7	2933	14	US-10-140-002-345	Sequence 345, App
20	579.8	95.7	2933	14	US-10-142-419-345	Sequence 345, App
21	579.8	95.7	2933	14	US-10-123-262-345	Sequence 345, App
22	579.8	95.7	2933	14	US-10-142-423-345	Sequence 345, App
23	579.8	95.7	2933	14	US-10-121-050-345	Sequence 345, App
24	579.8	95.7	2933	14	US-10-143-032-345	Sequence 345, App
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26	579.8	95.7	2933	14	US-10-123-261-345	Sequence 345, App
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31	579.8	95.7	2933	14	US-10-123-292-345	Sequence 345, App
32	579.8	95.7	2933	14	US-10-124-903-345	Sequence 345, App
33	579.8	95.7	2933	14	US-10-123-903-345	Sequence 345, App
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35	579.8	95.7	2933	14	US-10-124-822-345	Sequence 345, App
36	579.8	95.7	2933	14	US-10-160-925-345	Sequence 345, App
37	579.8	95.7	2933	14	US-10-160-498-345	Sequence 345, App
38	579.8	95.7	2933	14	US-10-124-824-345	Sequence 345, App
39	579.8	95.7	2933	14	US-10-127-829A-345	Sequence 345, App
40	579.8	95.7	2933	14	US-10-127-835A-345	Sequence 345, App
41	579.8	95.7	2933	14	US-10-127-839A-345	Sequence 345, App
42	579.8	95.7	2933	14	US-10-127-901A-345	Sequence 345, App
43	579.8	95.7	2933	14	US-10-128-693A-345	Sequence 345, App
44	579.8	95.7	2933	14	US-10-131-813A-345	Sequence 345, App
45	579.8	95.7	2933	14	US-10-131-813A-345	Sequence 345, App

ALIGNMENTS

RESULT 1
US-09-908-322-26
Sequence 26, Application US/09908322
Patent No. US20020107194A1
 GENERAL INFORMATION:
   APPLICANT: Ish-Horowicz, David
             Henrique, Domingos Manuel Pinto
             Lewis, Julian Hart
             Artavanis-Tsakonas, Spyridon
             Gray, Grace
   TITLE OF INVENTION: NUCLEOTIDE AND PROTEIN SEQUENCES OF
                       VERTEBRATE DELTA GENE AND METHODS BASED THEREON
   NUMBER OF SEQUENCES: 94
   CORRESPONDENCE ADDRESS:
     ADDRESSEE: Pennie & Edmonds LLP
     STREET: 1155 Avenue of the Americas
     CITY: New York
     STATE: NY
     COUNTRY: USA
     ZIP: 10036/2711
   COMPUTER READABLE FORM:
     MEDIUM TYPE: Diskette
     COMPUTER: IBM Compatible
     OPERATING SYSTEM: DOS
     SOFTWARE: FastSEQ Version 2.0
   CURRENT APPLICATION DATA:
     APPLICATION NUMBER: US/09/908,322
     FILING DATE: 17-Jul-2001
     CLASSIFICATION: <Unknown>
   PRIOR APPLICATION DATA:
     APPLICATION NUMBER: 08/981,392
     FILING DATE: 22-DEC-1997
   ATTORNEY/AGENT INFORMATION:
     NAME: Misrock, S Leslie
     REGISTRATION NUMBER: 18,872

~   REFERENCE/DOCKET NUMBER: 7326-123
~   TELECOMMUNICATION INFORMATION:
~   TELEPHONE: 212-790-9090
~   TELEFAX: 212-869-8864
~   TELEX: 66141 PENNIE
~   INFORMATION FOR SEQ ID NO: 26:
~   SEQUENCE CHARACTERISTICS:
~   LENGTH: 1981 base pairs
~   TYPE: nucleic acid
~   STRANDEDNESS: single
~   TOPOLOGY: linear
~   MOLECULE TYPE: cDNA
~   SEQUENCE DESCRIPTION: SEQ ID NO: 26:
US-09-908-322-26

Query Match   99.8%;   Score 605;   DB 9; Length 1981;
Best Local Similarity   100.0%; Pred. No. 2.4e-179;
Matches   606; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

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RESULT 2
US-09-783-931-26
; Sequence 26, Application US/09783931
; Publication No. US20030073620A1
; GENERAL INFORMATION:
    APPLICANT: Ish-Horowicz, David
        Henrique, Domingos Manuel Pinto
        Lewis, Julian Hart
        Artavanis-Tsakonas, Spyridon

~   Gray, Grace
    TITLE OF INVENTION: ANTIBODIES TO VERTEBRATE DELTA PROTEINS
                       AND FRAGMENTS
~   NUMBER OF SEQUENCES: 94
~   CORRESPONDENCE ADDRESS:
        ADDRESSEE: Pennie & Edmonds LLP
        STREET: 1155 Avenue of the Americas
        CITY: New York
        STATE: NY
        COUNTRY: USA
        ZIP: 10036/2711
~   COMPUTER READABLE FORM:
        MEDIUM TYPE: Diskette
        COMPUTER: IBM Compatible
        OPERATING SYSTEM: DOS
        SOFTWARE: FastSEQ Version 2.0
~   CURRENT APPLICATION DATA:
        APPLICATION NUMBER: US/09/783,931
        FILING DATE: 15-Feb-2001
        CLASSIFICATION: <Unknown>
~   PRIOR APPLICATION DATA:
        APPLICATION NUMBER: 08/981,392
        FILING DATE: 22-DEC-1997
~   ATTORNEY/AGENT INFORMATION:
        NAME: Antler, Adriane M.
        REGISTRATION NUMBER: 32,605
        REFERENCE/DOCKET NUMBER: 7326-122
~   TELECOMMUNICATION INFORMATION:
        TELEPHONE: 212-790-9090
        TELEFAX: 212-869-8864
        TELEX: 66141 PENNIE
~   INFORMATION FOR SEQ ID NO: 26:
        SEQUENCE CHARACTERISTICS:
            LENGTH: 1981 base pairs
            TYPE: nucleic acid
            STRANDEDNESS: single
            TOPOLOGY: linear
        MOLECULE TYPE: DNA
        SEQUENCE DESCRIPTION: SEQ ID NO: 26:
US-09-783-931-26

Query Match   99.8%;   Score 605;   DB 10; Length 1981;
Best Local Similarity   100.0%; Pred. No. 2.4e-179;
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OM nucleic - nucleic search, using sw model

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GenCore version 5.1.6

Run on: November 20, 2004, 14:51:01 ; Search time 72 Seconds
                                             (without alignments)
                                             5582.473 Million cell updates/sec

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Scoring table: IDENTITY_NUC
                Gapop 10.0 , Gapext 1.0
Searched: 824507 seqs, 355394441 residues

Total number of hits satisfying chosen parameters: 1649014

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :   Issued_Patents_NA:*
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                2: /cgn2_6/ptodata/1/1na/5B_COMB.seq:*
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                6: /cgn2_6/ptodata/1/1na/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Match Length	DB	DB ID	Description
1	605	99.8	1981	3	US-08-981-392-26	Sequence 26, Appl
2	605	99.8	1981	3	US-09-908-322-26	Sequence 26, Appl
3	579.8	95.7	2183	4	US-09-641-612-9	Sequence 9, Appl
4	579.8	95.7	2663	4	US-09-068-740A-8	Sequence 8, Appl
5	579.8	95.7	2663	4	US-09-423-753-8	Sequence 8, Appl
6	579.8	95.7	2933	4	US-10-140-002-345	Sequence 345, App
7	573	94.6	2899	3	US-08-981-392-24	Sequence 24, Appl
8	573	94.6	2899	3	US-09-908-322-24	Sequence 24, Appl
9	469.4	77.5	2508	4	US-08-981-392-1	Sequence 1, Appl
10	469.4	77.5	2508	4	US-09-908-322-1	Sequence 1, Appl
11	469.4	77.5	2883	3	US-08-981-392-3	Sequence 3, Appl
12	469.4	77.5	2883	3	US-09-908-322-3	Sequence 3, Appl
13	468.2	77.3	2692	3	US-08-981-392-11	Sequence 11, Appl
14	468.2	77.3	2692	4	US-09-908-322-11	Sequence 11, Appl
15	459.4	75.9	716	4	US-09-423-753-11	Sequence 11, Appl
16	457.4	75.5	2857	3	US-08-981-392-4	Sequence 4, Appl
17	457.4	75.5	2857	3	US-09-908-322-4	Sequence 4, Appl
18	220	36.3	2055	3	US-08-872-855-3	Sequence 3, Appl
19	220	36.3	2055	4	US-09-641-612-10	Sequence 10, Appl
20	220	36.3	2159	4	US-10-140-002-87	Sequence 87, Appl
21	220	36.3	2800	3	US-09-872-855-1	Sequence 1, Appl
22	220	36.3	3339	4	US-09-423-753-4	Sequence 4, Appl
23	220	36.3	2800	3	US-08-882-046-3	Sequence 3, Appl
24	178.8	29.5	4315	4	US-09-566-047-3	Sequence 3, Appl
25	178.8	29.5	2892	1	US-08-264-534-5	Sequence 5, Appl
26	178.6	29.5	2892	1	US-08-083-590A-1	Sequence 1, Appl
27	178.6	29.5	2892	1	US-08-465-500-5	Sequence 5, Appl
28	178.6	29.5	2892	2	US-08-346-126-5	Sequence 5, Appl
29	178.6	29.5	2892	2	US-08-346-128-5	Sequence 5, Appl
30	178.6	29.5	2892	3	US-08-532-384-1	Sequence 1, Appl
31	178.6	29.5	2892	3	US-08-893-828-5	Sequence 5, Appl
32	177.2	29.2	3955	3	US-09-214-278-4	Sequence 4, Appl
33	177.2	29.2	3955	3	US-09-855-722-4	Sequence 4, Appl
34	177.2	29.2	4464	2	US-08-400-159-7	Sequence 7, Appl
35	177.2	29.2	4483	2	US-08-611-729A-7	Sequence 7, Appl
36	177.2	29.2	4483	3	US-09-195-524-7	Sequence 7, Appl
37	161.8	26.7	4208	3	US-09-214-278-6	Sequence 6, Appl
38	161.8	26.7	4208	3	US-09-068-740A-10	Sequence 10, Appl
39	161.8	26.7	4208	3	US-09-855-722-6	Sequence 6, Appl
40	161.8	26.7	5590	4	US-08-882-046-1	Sequence 1, Appl
41	161.8	26.7	5590	4	US-09-566-047-1	Sequence 1, Appl
42	161.4	26.6	3201	4	US-09-579-536C-17	Sequence 17, Appl
43	161.4	26.6	3657	4	US-09-579-536C-2	Sequence 2, Appl
44	160.2	26.4	4855	4	US-09-917-254-34	Sequence 34, Appl
45	160.2	26.4	5458	4	US-09-199-865-2	Sequence 2, Appl

ALIGNMENTS

RESULT 1
US-08-981-392-26
; Sequence 26, Application US/08981392
; Patent No. 6262025
; GENERAL INFORMATION:
; APPLICANT: Ish-Horowicz, David
; APPLICANT: Henrique, Domingos Manuel Pinto
; APPLICANT: Lewis, Julian Hart
; APPLICANT: Artavanis-Tsakonas, Spyridon
; APPLICANT: Gray, Grace
; TITLE OF INVENTION: NUCLEOTIDE AND PROTEIN SEQUENCES
; TITLE OF INVENTION: OF VERTEBRATE DELTA GENES AND METHODS BASED THEREON
; NUMBER OF SEQUENCES: 94
; CORRESPONDENCE ADDRESS:
;   ADDRESSEE: Pennie & Edmonds LLP
;   STREET: 1155 Avenue of the Americas
;   CITY: New York
;   STATE: NY
;   COUNTRY: USA
;   ZIP: 10036/2711
; COMPUTER READABLE FORM:
;   MEDIUM TYPE: Diskette
;   COMPUTER: IBM Compatible
;   OPERATING SYSTEM: DOS
;   SOFTWARE: FastSEQ Version 2.0
; CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/08/981,392
;   FILING DATE: 22-DEC-1997
;   CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
;   NAME: Antler, Adriane M.
;   REGISTRATION NUMBER: 32,605
;   REFERENCE/DOCKET NUMBER: 7326-038
; TELECOMMUNICATION INFORMATION:
;   TELEPHONE: 212-790-9090
;   TELEFAX: 212-869-8864
;   TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 26:
;   SEQUENCE CHARACTERISTICS:
;   LENGTH: 1981 base pairs
;   TYPE: nucleic acid
;   STRANDEDNESS: single
;   TOPOLOGY: linear
;   MOLECULE TYPE: DNA
US-08-981-392-26

  Query Match   99.8%; Score 605; DB 3; Length 1981;
  Best Local Similarity   100.0%; Pred. No. 5.4e-170;
  Matches 606 Conservative   0; Mismatches   0; Indels   0; Gaps   0;

GENERAL INFORMATION:
APPLICANT: Ish-Horowicz, David
  Henrique, Domingos Manuel Pinto
  Lewis, Julian Hart
  Artavanis-Tsakonas, Spyridon
  Gray, Grace

TITLE OF INVENTION: NUCLEOTIDE AND PROTEIN SEQUENCES OF
  VERTEBRATE DELTA GENE AND METHODS BASED THEREON

NUMBER OF SEQUENCES: 94

CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: NY
COUNTRY: USA
ZIP: 10036/2711

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ Version 2.0

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/908,322
FILING DATE: 17-Jul-2001

CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/981,392
FILING DATE: 22-DEC-1997
ATTORNEY/AGENT INFORMATION:
NAME: Misrock, S Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 7326-123
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-790-9090
TELEFAX: 212-869-8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 26:
SEQUENCE CHARACTERISTICS:
LENGTH: 1981 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
SEQUENCE DESCRIPTION: SEQ ID NO: 26:
US-09-908-322-26

Query Match 99.8%; Score 605; DB 4; Length 1981;
Best Local Similarity 100.0%; Pred. No. 5.4e-170;
Matches 606; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 2
US-09-908-322-26
Sequence 26, Application US/09908322
Patent No. 6783956

Qy 1 GCTTCACCTGGCCGGGCACCTTCTTCTCTGATTATTGAAGCTCTCCACACAGATTCTCCTG 60
   ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 60 GCTTCACCTGGCCGGGCACCTTCTTCTCTGATTATTGAAGCTCTCCACACAGATTCTCCTG 119

Qy 61 ATGACCTGCAACAGAAAACCCAGAAAAGACTCATCAGCCGCGCGCCTGGCCACCCAGAGGCACC 120
   ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 120 ATGACCTGCAACAGAAAACCCAGAAAAGACTCATCAGCCGCGCGCCTGGCCACCCAGAGGCACC 179

Qy 121 TGACGGTGGGGCGGAGGAGTGGGTCCCAGGACCTGCACAGCAGAGCGGCGCACCTCAAGT 180
   ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 180 TGACGGTGGGGCGGAGGAGTGGGTCCCAGGACCTGCACAGCAGAGCGGCGCACCTCAAGT 239

Qy 181 ACTCCTACCGCTTCGTGTGTGACGAACACTACTACGGAGAGAGGAGAGGCGTCCGTTTTTCTGCC 240
   ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 240 ACTCCTACCGCTTCGTGTGTGACGAACACTACTACGGAGAGAGGAGAGGCGTCCGTTTTTCTGCC 299

Qy 241 GTCCCCGGGACGATGCCTTCGGCCCACTTCACCTGTGGGGGAGGCGTGGGGGAGAAAGTGTGCA 300
   ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 300 GTCCCCGGGACGATGCCTTCGGCCCACTTCACCTGTGGGGGAGGCGTGGGGGAGAAAGTGTGCA 359

Qy 301 ACCCTGGCTGGAAAGGGCCCTACTGCACAGAGAGCGGATCTGCCCTGGATGTGATGAGC 360
   ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 360 ACCCTGGCTGGAAAGGGCCCTACTGCACAGAGAGCGGATCTGCCCTGGATGTGATGAGC 419

Qy 361 AGCATGGATTTTGTGACAAACCAGGGGAATGCAAGTGCAGAGTGGGCGTTGGCAGGGCCGGT 420
   ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 420 AGCATGGATTTTGTGACAAACCAGGGGAATGCAAGTGCAGAGTGGGCGTTGGCAGGGCCGGT 479

Qy 421 ACTGTGACGAGTGTATCCGCTATCCAGGCTGTCTCCATGGCACCTGCCAGCAGCCCCTGGC 480
   ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 480 ACTGTGACGAGTGTATCCGCTATCCAGGCTGTCTCCATGGCACCTGCCAGCAGCCCCTGGC 539

Qy 481 AGTGCAACTGCCAGGAAGGNTGGGGGGGGCCTTTTCTGCAACCAGGACCTGAACTACTGCA 540
   ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 540 AGTGCAACTGCCAGGAAGGNTGGGGGGGGCCTTTTCTGCAACCAGGACCTGAACTACTGCA 599

Qy 541 CACACCATAAGCCCTGCAAGAAATGGAGCCACCTGCACCTGCAGCAGCCCTGGC 600
   ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 600 CACACCATAAGCCCTGCAAGAAATGGAGCCACCTGCACCTGCAGCAGCCCTGGC 659

Qy 601 CACTTG 606
   ||||||
Db 660 CACTTG 665

RESULT 3
US-09-641-612-9